

Exhibit A

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2006, 09:38:33 ; Search time 4463 Seconds
(without alignments)
1641.370 Million cell updates/sec

Title: US-10-604-985A-1

Sequence: 1 tggggccggggcatttgat.....gtatgcatcgacacacta 131

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est3:
3: gb_est4:
4: gb_est5:
5: gb_est6:
6: gb_hic:
7: gb_est2:
8: gb_est7:
9: gb_est8:
10: gb_est9:
11: gb_gsa1:
12: gb_gsa2:
13: gb_gsa3:
14: gb_gsa4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	131	100.0	766 1	AA878312 o661f09.8
2	36.4	27.8	508 2	BI295661 UI-R-DK0-
3	35	26.7	349 10	R61279 yhl0910.s1
4	34.8	26.6	536 7	BF401563 UI-R-CA0-
5	34.4	26.3	529 1	AI091085 qa53e12.8
6	33.4	25.5	529 1	AA723562 a242b08.8
7	32.6	24.9	504 1	AA411048 zva0c09.8
8	32.6	24.9	645 4	CA449806 UI-H-B11-
9	32.4	24.7	713 1	AA843803 ak09b09.8
10	32.4	24.6	435 1	AA46312 v87d06.y
11	32.2	24.6	447 1	AA763117 v87d06.y
12	32.2	24.6	457 7	BB818345 BB818345
13	32.2	24.6	467 1	AI003571 a188c10.8
14	32.2	24.6	714 4	BY734521 BY734521
15	32.2	24.6	785 6	AK144859 Mus muscu
16	31	23.7	152 3	BQ326113 MR2-CN003
17	31	23.7	276 10	T29822 EST96637 Hu
18	31	23.7	422 1	AI860196 wk97f02.x
19	31	23.7	438 4	CA433359 UI-H-CO0-

20	31	23.7	454 1	AI051116
21	31	23.7	510 3	BM710193
22	31	23.7	527 1	AA777651
23	31	23.7	545 3	BM671614
24	31	23.7	550 10	W39186
25	31	23.7	551 4	EX090074
26	31	23.7	563 9	DB370485
27	31	23.7	571 7	AA951613
28	31	23.7	572 1	AI057542
29	31	23.7	613 4	CB322052
30	31	23.7	620 1	AI807276
31	31	23.7	765 9	CX757568
32	31	23.7	939 1	AA843957
33	31	23.7	965 14	CNS07AC4
34	31	23.7	2849 14	DO046178
35	31	23.7	2849 14	DO046179
36	30.4	23.2	560 11	AQ073498
37	30.4	23.2	632 11	AG218808
38	30.2	23.1	324 8	CV316869
39	30	22.9	675 4	CB843988
40	29.8	22.7	140 7	AA895165
41	29.8	22.7	507 1	AA682887
42	29.4	22.4	352 10	DM313226
43	29.4	22.4	416 4	BY434683
44	29.4	22.4	416 4	BY434683
45	29.4	22.4	568 4	CA812289

ALIGNMENTS

RESULT 1
AA878312
LOCUS
DEFINITION
o661f09.s1 NCI CGAP LUS Homo sapiens CDNA clone IMAGE:1416137 3.
similar to gb:M18391 TYROSINE-PROTEIN KINASE RECEPTOR BPH PRECURSOR (HUMAN) ; mRNA sequence.

ACCESSION
AA878312.1 GI:2987277
VERSION
AA878312.1
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 766)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA library preparation: M. Bento Soares, Ph.D.
CDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/INM at:
www.bio.lnl.gov/bhrp/image/image.html
Insert Length: 712 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amerham
High quality sequence stop: 270.
Location/Qualifiers
1..766
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/db_xref="taxon:9606"
/clone="IMAGE:1416137"
/issue_type="carcinoid"
/lab_host="DH10B"
/clone_lhb="NCI CGAP LUS"
/note="Organ: lung; Vector: pT73D-Pac1, 1st strand cDNA